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<110> Kwang , Jimmy
 Ling, Ai Ee
 Ooi, Eng Eong
 Chng, Hiok Hee

<120> Diagnostics and Vaccines for SARS

<130> 2577-162

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 <141> 2003-07-15

<160> 25

<170> PatentIn version 3.2

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<213> SARS coronavirus

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 Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
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cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta ccc aat 144
 Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
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aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag gag gaa 192
 Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
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ctt aga ttc cct cga ggc cag ggc gtt cca atc aac acc aat agt ggt 240
 Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
 65 70 75 80

cca gat gac caa att ggc tac tac cga aga gct acc cga cga gtt cgt 288
 Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
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ggt ggt gac ggc aaa atg aaa gag ctc agc ccc aga tgg tac ttc tat 336
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gac cac att ggc acc cgc aat cct aat aac aat gct gcc acc gtg cta Asp His Ile Gly Thr Arg Asn Pro Asn Asn Ala Ala Thr Val Leu 145	150	155	480
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gct cga atg gct agc gga ggt ggt gaa act gcc ctc gcg cta ttg ctg Ala Arg Met Ala Ser Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu 210	215	220	672
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Ala	Ile	Lys	Leu	Asp	Asp	Lys	Asp	Pro	Gln	Phe	Lys	Asp	Asn	Val	Ile	
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cct aaa aag gac aaa aag aaa aag act gat gaa gct cag cct ttg ccg															1152	
Pro	Lys	Lys	Asp	Lys	Lys	Thr	Asp	Glu	Ala	Gln	Pro	Leu	Pro			
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Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu																
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Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly																
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115 120 125

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Asp His Ile Gly Thr Arg Asn Pro Asn Asn Ala Ala Thr Val Leu
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Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
165 170 175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
180 185 190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
195 200 205

Ala Arg Met Ala Ser Gly Gly Glu Thr Ala Leu Ala Leu Leu
210 215 220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
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Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
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260 265 270

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275 280 285

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Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
 325 330 335

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Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
 355 360 365

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 Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
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 His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
 35 40 45

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65 70 75 80	
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115 120 125	
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165 170 175	
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180 185 190	
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195 200 205	
cta cct tct ggt ttt aac act ttg aaa cct att ttt aag ttg cct ctt Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu	672
210 215 220	
ggc att aac att aca aat ttt aga gcc att ctt aca gcc ttt tca cct Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro	720
225 230 235 240	
gct caa gac att tgg ggc acg tca gct gca gcc tat ttt gtt ggc tat Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr	768
245 250 255	
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ttc agg gtt gtt ccc tca gga gat gtt gtg aga ttc cct aat att aca Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr 305	310	315	960
aac ttg tgt cct ttt gga gag gtt ttt aat gct act aaa ttc cct tct Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser 325	330	335	1008
gtc tat gca tgg gag aga aaa aaa att tct aat tgt gtt gct gat tac Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr 340	345	350	1056
tct gtg ctc tac aac tca aca ttt ttt tca acc ttt aag tgc tat ggc Ser Val Leu Tyr Asn Ser Thr Phe Ser Thr Phe Lys Cys Tyr Gly 355	360	365	1104
gtt tct gcc act aag ttg aat gat ctt tgc ttc tcc aat gtc tat gca Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala 370	375	380	1152
gat tct ttt gta gtc aag gga gat gat gta aga caa ata gcg cca gga Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly 385	390	395	1200
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atg ggt tgt gtc ctt gct tgg aat act agg aac att gat gct act tca Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser 420	425	430	1296
act ggt aat tat aat tat aaa tat agg tat ctt aga cat ggc aag ctt Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu 435	440	445	1344
agg ccc ttt gag aga gac ata tct aat gtg cct ttc tcc cct gat ggc Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly 450	455	460	1392
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tat ggt ttt tac acc act act ggc att ggc tac caa cct tac aga gtt			1488

Tyr	Gly	Phe	Tyr	Thr	Thr	Thr	Gly	Ile	Gly	Tyr	Gln	Pro	Tyr	Arg	Val	
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Val	Val	Leu	Ser	Phe	Glu	Leu	Leu	Asn	Ala	Pro	Ala	Thr	Val	Cys	Gly	
500							505				510					
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Pro	Lys	Leu	Ser	Thr	Asp	Leu	Leu	Lys	Asn	Gln	Cys	Val	Asn	Phe	Asn	
515							520				525					
ttt	aat	gga	ctc	act	ggt	act	ggt	gtg	tta	act	cct	tct	tca	aag	aga	1632
Phe	Asn	Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Pro	Ser	Ser	Lys	Arg	
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Ser	Val	Arg	Asp	Pro	Lys	Thr	Ser	Glu	Ile	Leu	Asp	Ile	Ser	Pro	Cys	
565							570				575					
tct	ttt	ggg	ggt	gta	agt	gta	att	aca	cct	gga	aca	aat	gct	tca	tct	1776
Ser	Phe	Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Ala	Ser	Ser	
580							585				590					
gaa	gtt	gct	gtt	cta	tat	caa	gat	gtt	aac	tgc	act	gat	gtt	tct	aca	1824
Glu	Val	Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Asp	Val	Ser	Thr	
595							600				605					
gca	att	cat	gca	gat	caa	ctc	aca	cca	gct	tgg	cgc	ata	tat	tct	act	1872
Ala	Ile	His	Ala	Asp	Gln	Leu	Thr	Pro	Ala	Trp	Arg	Ile	Tyr	Ser	Thr	
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gga	aac	aat	gta	ttc	cag	act	caa	gca	ggc	tgt	ctt	ata	gga	gct	gag	1920
Gly	Asn	Asn	Val	Phe	Gln	Thr	Gln	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	
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cat	gtc	gac	act	tct	tat	gag	tgc	gac	att	cct	att	gga	gct	ggc	att	1968
His	Val	Asp	Thr	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	
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tgt	gct	agt	tac	cat	aca	gtt	tct	tta	tta	cgt	agt	act	agc	caa	aaa	2016
Cys	Ala	Ser	Tyr	His	Thr	Val	Ser	Leu	Leu	Arg	Ser	Thr	Ser	Gln	Lys	
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Ser	Ile	Val	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Asp	Ser	Ser	Ile	Ala	
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Tyr	Ser	Asn	Asn	Thr	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Ser	Ile	Ser	Ile	
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Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu					
caa tat ggt agc ttt tgc aca caa cta aat cgt gca ctc tca ggt att	740	745	750		2256
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile					
gct gct gaa cag gat cgc aac aca cgt gaa gtg ttc gct caa gtt aaa	755	760	765		2304
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys					
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Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe.					
tca caa ata tta cct gac cct cta aag cca act aag agg tct ttt att	785	790	795	800	2400
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile					
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Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met					
aag caa tat ggc gaa tgc cta ggt gat att aat gct aga gat ctc att	820	825	830		2496
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile					
tgt gcg cag aag ttc aat gga ctt aca gtg ttg cca cct ctg ctc act	835	840	845		2544
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr					
gat gat atg att gct gcc tac act gct gct cta gtt agt ggt act gcc	850	855	860		2592
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala					
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Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe					
gct atg caa atg gca tat agg ttc aat ggc att gga gtt acc caa aat	885	890	895		2688
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn					
gtt ctc tat gag aac caa aaa caa atc gcc aac caa ttt aac aag gcg	900	905	910		2736
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala					
att agt caa att caa gaa tca ctt aca aca aca tca act gca ttg ggc	915	920	925		2784
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Ser Thr Ala Leu Gly					

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Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu	
930 935 940	
gtt aaa caa ctt agc tct aat ttt ggt gca att tca agt gtg cta aat	2880
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn	
945 950 955 960	
gat atc ctt tcg cga ctt gat aaa gtc gag gcg gag gta caa att gac	2928
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp	
965 970 975	
agg tta att aca ggc aga ctt caa agc ctt caa acc tat gta aca caa	2976
Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln	
980 985 990	
caa cta atc agg gct gct gaa atc agg gct tct gct aat ctt gct gct	3024
Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala	
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Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser	
1070 1075 1080	
tgg ttt att aca cag agg aac ttc ttt tct cca caa ata att act	3294
Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr	
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atc att aac aac aca gtt tat gat cct ctg caa cct gag ctt gac	3384
Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp	
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Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser	

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cca gat	gtt gat ctt ggc gac	att tca ggc att aac	gct tct gtc	3474
Pro Asp	Val Asp Leu Gly Asp	Ile Ser Gly Ile Asn	Ala Ser Val	
1145	1150	1155		
gtc aac	att caa aaa gaa att	gac cgc ctc aat gag	gtc gct aaa	3519
Val Asn	Ile Gln Lys Glu Ile	Asp Arg Leu Asn Glu	Val Ala Lys	
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aat tta	aat gaa tca ctc att	gac ctt caa gaa ttg	gga aaa tat	3564
Asn Leu	Asn Glu Ser Leu Ile	Asp Leu Gln Glu Leu	Gly Lys Tyr	
1175	1180	1185		
gag caa	tat att aaa tgg cct	tgg tat gtt tgg ctc	ggc ttc att	3609
Glu Gln	Tyr Ile Lys Trp Pro	Trp Tyr Val Trp Leu	Gly Phe Ile	
1190	1195	1200		
gct gga	cta att gcc atc gtc	atg gtt aca atc ttg	ctt tgt tgc	3654
Ala Gly	Leu Ile Ala Ile Val	Met Val Thr Ile Leu	Leu Cys Cys	
1205	1210	1215		
atg act	agt tgt tgc agt tgc	ctc aag ggt gca tgc	tct tgt ggt	3699
Met Thr	Ser Cys Cys Ser Cys	Leu Lys Gly Ala Cys	Ser Cys Gly	
1220	1225	1230		
tct tgc	tgc aag ttt gat gag	gat gac tct gag cca	gtt ctc aag	3744
Ser Cys	Cys Lys Phe Asp Glu	Asp Asp Ser Glu Pro	Val Leu Lys	
1235	1240	1245		
ggt gtc	aaa tta cat tac aca	taa		3768
Gly Val	Lys Leu His Tyr Thr			
1250	1255			

<210> 4

<211> 1255

<212> PRT

<213> SARS coronavirus

<400> 4

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu			
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Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln		
20	25	30

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg		
35	40	45

Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser		
---	--	--

50

55

60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
195 200 205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
210 215 220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225 230 235 240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
245 250 255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
260 265 270

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
275 280 285

Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
290 295 300

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305 310 315 320

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
325 330 335

Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
340 345 350

Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
355 360 365

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
370 375 380

Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385 390 395 400

Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
405 410 415

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
420 425 430

Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
435 440 445

Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
450 455 460

Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465 470 475 480

Tyr Gly Phe Tyr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
485 490 495

Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
500 505 510

Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
515 520 525

Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
530 535 540

Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545 550 555 560

Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
565 570 575

Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590

Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
595 600 605

Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
610 615 620

Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625 630 635 640

His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
645 650 655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
660 665 670

Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
675 680 685

Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
690 695 700

Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705 710 715 720

Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
725 730 735

Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
740 745 750

Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
755 760 765

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
770 775 780

Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785 790 795 800

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
805 810 815

Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
820 825 830

Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
835 840 845

Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
850 855 860

Thr Ala Gly Trp Thr Phe Gly Ala Ala Leu Gln Ile Pro Phe
865 870 875 880

Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
885 890 895

Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
900 905 910

Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Ser Thr Ala Leu Gly
915 920 925

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu

930

935

940

Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945 950 955 960

Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
965 970 975

Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
980 985 990

Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
995 1000 1005

Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
1010 1015 1020

Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala
1025 1030 1035

Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
1040 1045 1050

Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
1055 1060 1065

Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
1070 1075 1080

Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr
1085 1090 1095

Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
1100 1105 1110

Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
1115 1120 1125

Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
1130 1135 1140

Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
 1145 1150 1155

Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys
 1160 1165 1170

Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
 1175 1180 1185

Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Val Trp Leu Gly Phe Ile
 1190 1195 1200

Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Leu Leu Cys Cys
 1205 1210 1215

Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys Gly
 1220 1225 1230

Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
 1235 1240 1245

Gly Val Lys Leu His Tyr Thr
 1250 1255

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 <211> 588
 <212> DNA
 <213> SARS coronavirus

<220>
 <221> CDS
 <222> (1)..(588)

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 Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln Gln Gln
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ggc caa act gtc act aag aaa tct gct gct gag gca tct aaa aag cct 96
 Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser Lys Lys Pro
 20 25 30

cgc caa aaa cgt act gcc aca aaa cag tac aac gtc act caa gca ttt 144
 Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr Gln Ala Phe
 35 40 45

ggg aga cgt ggt cca gaa caa acc caa gga aat ttc ggg gac caa gac	50	55	60	192	
Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly Asp Gln Asp					
cta atc aga caa gga act gat tac aaa cat tgg ccg caa att gca caa	65	70	75	240	
Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln Ile Ala Gln					
ttt gct cca agt gcc tct gca ttc ttt gga atg tca cgc att ggc atg	85	90	95	288	
Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg Ile Gly Met					
gaa gtc aca cct tcg gga aca tgg ctg act tat cat gga gcc att aaa	100	105	110	336	
Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly Ala Ile Lys					
ttg gat gac aaa gat cca caa ttc aaa gac aac gtc ata ctg ctg aac	115	120	125	384	
Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile Leu Leu Asn					
aag cac att gac gca tac aaa aca ttc cca cca aca gag cct aaa aag	130	135	140	432	
Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu Pro Lys Lys					
gac aaa aag aaa aag act gat gaa gct cag cct ttg ccg cag aga caa	145	150	155	480	
Asp Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro Gln Arg Gln					
aag aag cag ccc act gtg act ctt ctt cct gcg gct gac atg gat gat	165	170	175	528	
Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp Met Asp Asp					
ttc tcc aga caa ctt caa aat tcc atg agt gga gct tct gct gat tca	180	185	190	576	
Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser Ala Asp Ser					
act cag gca taa				588	
Thr Gln Ala					
195					
<210> 6					
<211> 195					
<212> PRT					
<213> SARS coronavirus					
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Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln Gln Gln	1	5	10	15	
Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser Lys Lys Pro	20	25	30		

Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr Gln Ala Phe
35 40 45

Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly Asp Gln Asp
50 55 60

Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln Ile Ala Gln
65 70 75 80

Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg Ile Gly Met
85 90 95

Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly Ala Ile Lys
100 105 110

Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile Leu Leu Asn
115 120 125

Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu Pro Lys Lys
130 135 140

Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro Gln Arg Gln
145 150 155 160

Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp Met Asp Asp
165 170 175

Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser Ala Asp Ser
180 185 190

Thr Gln Ala
195

<210> 7
<211> 684
<212> DNA
<213> SARS coronavirus

<220>
<221> CDS
<222> (1)..(684)

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 Arg Tyr Leu Arg His Gly Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser
 1 5 10 15

aat gtg cct ttc tcc cct gat ggc aaa cct tgc acc cca cct gct ctt 96
 Asn Val Pro Phe Ser Pro Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu
 20 25 30

aat tgt tat tgg cca tta aat gat tat ggt ttt tac acc act act ggc 144
 Asn Cys Tyr Trp Pro Leu Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly
 35 40 45

att ggc tac caa cct tac aga gtt gta gta ctt tct ttt gaa ctt tta 192
 Ile Gly Tyr Gln Pro Tyr Arg Val Val Leu Ser Phe Glu Leu Leu
 50 55 60

aat gca ccg gcc acg gtt tgt gga cca aaa tta tcc act gac ctt att 240
 Asn Ala Pro Ala Thr Val Cys Gly Pro Lys Leu Ser Thr Asp Leu Ile
 65 70 75 80

aag aac cag tgt gtc aat ttt aat gga ctc act ggt act ggt 288
 Lys Asn Gln Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
 85 90 95

gtg tta act cct tct tca aag aga ttt caa cca ttt caa caa ttt ggc 336
 Val Leu Thr Pro Ser Ser Lys Arg Phe Gln Pro Phe Gln Gln Phe Gly
 100 105 110

cgt gat gtt tct gat ttc act gat tcc gtt cga gat cct aaa aca tct 384
 Arg Asp Val Ser Asp Phe Thr Asp Ser Val Arg Asp Pro Lys Thr Ser
 115 120 125

gaa ata tta gac att tca cct tgc tct ttt ggg ggt gta agt gta att 432
 Glu Ile Leu Asp Ile Ser Pro Cys Ser Phe Gly Gly Val Ser Val Ile
 130 135 140

aca cct gga aca aat gct tca tct gaa gtt gct cta tat caa gat 480
 Thr Pro Gly Thr Asn Ala Ser Ser Glu Val Ala Val Leu Tyr Gln Asp
 145 150 155 160

gtt aac tgc act gat gtt tct aca gca att cat gca gat caa ctc aca 528
 Val Asn Cys Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr
 165 170 175

cca gct tgg cgc ata tat tct act gga aac aat gta ttc cag act caa 576
 Pro Ala Trp Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln
 180 185 190

gca ggc tgt ctt ata gga gct gag cat gtc gac act tct tat gag tgc 624
 Ala Gly Cys Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys
 195 200 205

gac att cct att gga gct ggc att tgt gct agt tac cat aca gtt tct 672
 Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser

210

215

220

tta tta cgt agt
Leu Leu Arg Ser
225

684

<210> 8
<211> 228
<212> PRT
<213> SARS coronavirus

<400> 8

Arg Tyr Leu Arg His Gly Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser
1 5 10 15

Asn Val Pro Phe Ser Pro Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu
20 25 30

Asn Cys Tyr Trp Pro Leu Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly
35 40 45

Ile Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu
50 55 60

Asn Ala Pro Ala Thr Val Cys Gly Pro Lys Leu Ser Thr Asp Leu Ile
65 70 75 80

Lys Asn Gln Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
85 90 95

Val Leu Thr Pro Ser Ser Lys Arg Phe Gln Pro Phe Gln Gln Phe Gly
100 105 110

Arg Asp Val Ser Asp Phe Thr Asp Ser Val Arg Asp Pro Lys Thr Ser
115 120 125

Glu Ile Leu Asp Ile Ser Pro Cys Ser Phe Gly Gly Val Ser Val Ile
130 135 140

Thr Pro Gly Thr Asn Ala Ser Ser Glu Val Ala Val Leu Tyr Gln Asp
145 150 155 160

Val Asn Cys Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr

165

170

175

Pro Ala Trp Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln
 180 185 190

Ala Gly Cys Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys
 195 200 205

Asp Ile Pro Ilé Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser
 210 215 220

Leu Leu Arg Ser
 225

<210> 9
 <211> 29711
 <212> DNA
 <213> SARS coronavirus

<400> 9
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 900

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ctgcgcgtg tatgcgttct cttaaagctc ctgcccgtat gtcagtatca tcaccagatg	4620
ctgttactac atataatgga tacctcactt cgtcatcaaa gacatctgag gaggcacttg	4680
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